

SEQUENCE LISTING

<110> Hepgenics Pty Ltd

<120> VIRAL VECTORS EXPRESSING FUSION OF VIRAL LARGE ENVELOPE
PROTEIN AND PROTEIN OF INTEREST

<130> 19242

<140> 10/553,683

<141> 2005-10-17

<150> AU 2003901876

<151> 2003-04-17

<160> 13

<170> PatentIn version 3.2

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<213> duck

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34

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<211> 3021

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 <212> DNA
 <213> duck

<220>
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 <222> (1)..(984)

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1				5				10					15					
gga	gaa	ata	ctg	tta	aac	caa	ctt	gcc	gga	agg	atg	atc	cca	aaa	ggg	96		
Gly	Glu	Ile	Leu	Leu	Asn	Gln	Leu	Ala	Gly	Arg	Met	Ile	Pro	Lys	Gly			
20				25					30									
act	ttg	aca	tgg	tca	ggc	aag	ttt	cca	aca	ctt	gat	cac	gt	tta	gac	144		
Thr	Leu	Thr	Trp	Ser	Gly	Lys	Phe	Pro	Thr	Leu	Asp	His	Val	Leu	Asp			
35				40					45									
cat	gtg	caa	aca	atg	gag	gag	ata	aac	acc	ctc	cag	aat	cag	gga	gct	192		
His	Val	Gln	Thr	Met	Glu	Glu	Ile	Asn	Thr	Leu	Gln	Asn	Gln	Gly	Ala			
50				55					60									
tgg	cct	gct	ggg	g	cg	g	g	ag	ag	gt	g	ta	aa	cc	act	cct	240	

Trp	Pro	Ala	Gly	Ala	Gly	Arg	Arg	Val	Gly	Leu	Ser	Asn	Pro	Thr	Pro	65	70	75	80	
caa	gag	att	cct	cag	ccc	cag	tgg	act	ccc	gag	gaa	gac	caa	aaa	gca					288
Gln	Glu	Ile	Pro	Gln	Pro	Gln	Trp	Thr	Pro	Glu	Glu	Asp	Gln	Lys	Ala					
				85				90					95							
cgc	gaa	gct	ttt	cgc	cgt	tat	caa	gaa	gaa	aga	cca	ccg	gaa	acc	acc					336
Arg	Glu	Ala	Phe	Arg	Arg	Tyr	Gln	Glu	Glu	Arg	Pro	Pro	Glu	Thr	Thr					
				100				105				110								
acc	att	cct	ccg	tct	tcc	cct	cag	tgg	aag	cta	caa	ccc	ggg	gac					384	
Thr	Ile	Pro	Pro	Ser	Ser	Pro	Gln	Trp	Lys	Leu	Gln	Pro	Gly	Asp						
				115				120			125									
gat	cca	ctc	ctg	gga	aat	cag	tct	ctc	ctc	gag	act	cat	ccg	cta	tac					432
Asp	Pro	Leu	Leu	Gly	Asn	Gln	Ser	Leu	Leu	Glu	Thr	His	Pro	Leu	Tyr					
				130				135			140									
cag	tca	gaa	cca	gcg	gtg	cca	gtg	ata	aaa	act	ccc	ccc	ttg	aag	aag					480
Gln	Ser	Glu	Pro	Ala	Val	Pro	Val	Ile	Lys	Thr	Pro	Pro	Leu	Lys	Lys					
				145				150			155			160						
aaa	atg	tct	ggt	acc	ttc	ggg	gga	ata	cta	gct	ggc	cta	atc	gga	tta					528
Lys	Met	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	Ala	Gly	Leu	Ile	Gly	Leu					
				165				170			175									
ctg	gta	agc	ttt	ttc	ttg	ttg	ata	aaa	att	cta	gaa	ata	ctg	agg	agg					576
Leu	Val	Ser	Phe	Phe	Leu	Leu	Ile	Lys	Ile	Leu	Glu	Ile	Leu	Arg	Arg					
				180				185			190									
cta	gat	tgg	tgg	tgg	att	tct	ctc	agt	tct	cca	aag	gga	aaa	atg	caa					624
Leu	Asp	Trp	Trp	Trp	Ile	Ser	Leu	Ser	Ser	Pro	Lys	Gly	Lys	Met	Gln					
				195				200			205									
tgc	gct	ttc	caa	gat	act	gga	gcc	caa	atc	tct	cca	cat	tac	gta	gga					672
Cys	Ala	Phe	Gln	Asp	Thr	Gly	Ala	Gln	Ile	Ser	Pro	His	Tyr	Val	Gly					
				210				215			220									
tct	tgc	ccg	tgg	gga	tgc	cca	gga	ttt	ctt	tgg	acc	tat	ctc	agg	ctt					720
Ser	Cys	Pro	Trp	Gly	Cys	Pro	Gly	Phe	Leu	Trp	Thr	Tyr	Leu	Arg	Leu					
				225				230			235			240						
ttt	atc	atc	ttc	ctc	tta	atc	ctg	cta	gta	gca	gca	ggc	ttg	ctg	tat					768
Phe	Ile	Ile	Phe	Leu	Ile	Leu	Ile	Leu	Val	Ala	Ala	Gly	Leu	Leu	Tyr					
				245				250			255									
ctg	acg	gac	aac	ggg	tct	act	att	tta	gga	aag	ctc	caa	tgg	gcg	tcg					816
Leu	Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser					
				260				265			270			270						
gtc	tca	gcc	ctt	ttc	tcc	tcc	atc	tct	tca	cta	ctg	ccc	tcg	gat	ccg					864
Val	Ser	Ala	Leu	Phe	Ser	Ser	Ile	Ser	Ser	Leu	Leu	Leu	Pro	Ser	Asp	Pro				
				275				280			285									
aaa	tct	ctc	gtc	gct	tta	acg	ttt	gga	ctt	tca	ctt	ata	tgg	atg	act					912
Lys	Ser	Leu	Val	Ala	Leu	Thr	Phe	Gly	Leu	Ser	Leu	Ile	Trp	Met	Thr					
				290				295			300									
tcc	tcc	tct	gcc	acc	caa	acg	ctc	gtc	acc	tta	acg	caa	tta	gcc	acg					960
Ser	Ser	Ser	Ala	Thr	Gln	Thr	Leu	Val	Thr	Leu	Thr	Gln	Leu	Ala	Thr					
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Leu Ser Ala Leu Phe Tyr Lys Ser
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<400> 7

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Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly
20 25 30

Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp
35 40 45

His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala
50 55 60

Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro
65 70 75 80

Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala
85 90 95

Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr
100 105 110

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp
115 120 125

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
130 135 140

Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
145 150 155 160

Lys Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu
165 170 175

Leu Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg
180 185 190

Leu Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln
195 200 205

Cys Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly
5

210

215

220

Ser Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu
225 230 235 240

Phe Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr
245 250 255

Leu Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser
260 265 270

Val Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro
275 280 285

Lys Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr
290 295 300

Ser Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr
305 310 315 320

Leu Ser Ala Leu Phe Tyr Lys Ser
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<210> 8
<211> 501
<212> DNA
<213> duck

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gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta 96
Val Ser Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu
20 25 30

gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc 144
Asp Trp Trp Trp Ile Ser Leu Ser Pro Lys Gly Lys Met Gln Cys
35 40 45

gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct 192
Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser
50 55 60

tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt 240
Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe
65 70 75 80

atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg 288
Ile Ile Phe Leu Leu Ile Leu Val Ala Ala Gly Leu Leu Tyr Leu
6

85	90	95	
acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc			336
Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val			
100	105	110	
tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg aaa			384
Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys			
115	120	125	
tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act tcc			432
Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser			
130	135	140	
tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg ctg			480
Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu			
145	150	155	160
tct gct ctt ttt tac aag agt			501
Ser Ala Leu Phe Tyr Lys Ser			
165			

<210> 9
<211> 167
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<400> 9

Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu
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Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu
20 25 30

Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys
35 40 45

Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser
50 55 60

Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe
65 70 75 80

Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu
85 90 95

Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val
100 105 110

Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys
115 120 125

Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser
130 135 140

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu
145 150 155 160

Ser Ala Leu Phe Tyr Lys Ser
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act ttg aca tgg tca ggc aag ttt cca aca cta gat cac gtg tta gac Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp 35 40 45	144
cat gtg caa aca atg gag gag ata aac acc ctc cag aat cag gga gct His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala 50 55 60	192
tgg cct gct ggg gcg gga agg aga gta gga tta tca aat ccg act cct Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro 65 70 75 80	240
caa gag att cct cag ccc cag tgg act ccc gag gaa gac caa aaa gca Gln Glu Ile Pro Gln Pro Trp Thr Pro Glu Glu Asp Gln Lys Ala 85 90 95	288
cgc gaa gct ttt cgc cgt tat caa gaa gaa aga cca ccg gaa acc acc Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr 100 105 110	336
acc att cct ccg tct tcc cct cct cag tgg aag cta caa ccc ggg gac Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp 115 120 125	384
gat cca ctc ctg gga aat cag tct ctc ctc gag act cat ccg cta tac Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr 130 135 140	432
cag tca gaa cca gcg gtg cca gtg ata aaa act ccc ccc ttg aag aag Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys 145 150 155 160	480
aaa Lys	483

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<212> PRT
<213> duck

<400> 11

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Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly
20 25 30

Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp
35 40 45

His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala
50 55 60

Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro
65 70 75 80

Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala
85 90 95

Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr
100 105 110

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp
115 120 125

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
130 135 140

Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
145 150 155 160

Lys

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<220>
<221> CDS
<222> (1)..(501)

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gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys 35 40 45	144
gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser 50 55 60	192
tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe 65 70 75 80	240
atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg Ile Ile Phe Leu Leu Ile Leu Val Ala Ala Gly Leu Leu Tyr Leu 85 90 95	288
acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val 100 105 110	336
tca gcc ctt ttc tcc atc tct tca cta ctg ccc tcg gat ccg aaa Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys 115 120 125	384
tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act tcc Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser 130 135 140	432
tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg ctg Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu 145 150 155 160	480
tct gct ctt ttt tac aag agt Ser Ala Leu Phe Tyr Lys Ser 165	501

<210> 13
<211> 167
<212> PRT
<213> duck

<400> 13

Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu
1 5 10 15

Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu
20 25 30

Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys
35 40 45

Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser
50 55 60

Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe
65 70 75 80

Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu
85 90 95

Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val
100 105 110

Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys
115 120 125

Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser
130 135 140

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu
145 150 155 160

Ser Ala Leu Phe Tyr Lys Ser
165